

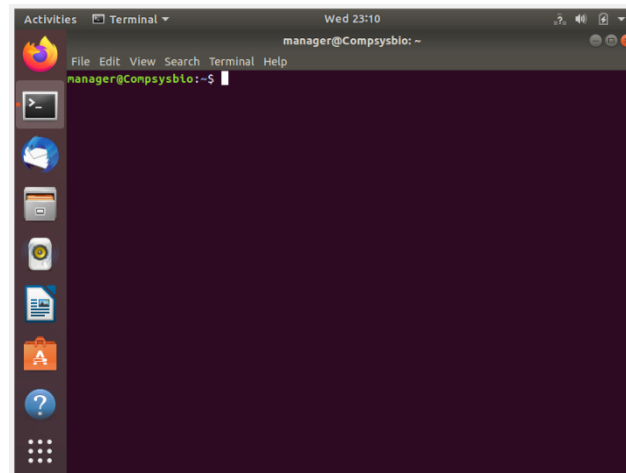
WGCAC Computational Systems Biology for Complex
Human Disease 4- 9 December 2022

Instructors: Anna Niarakis

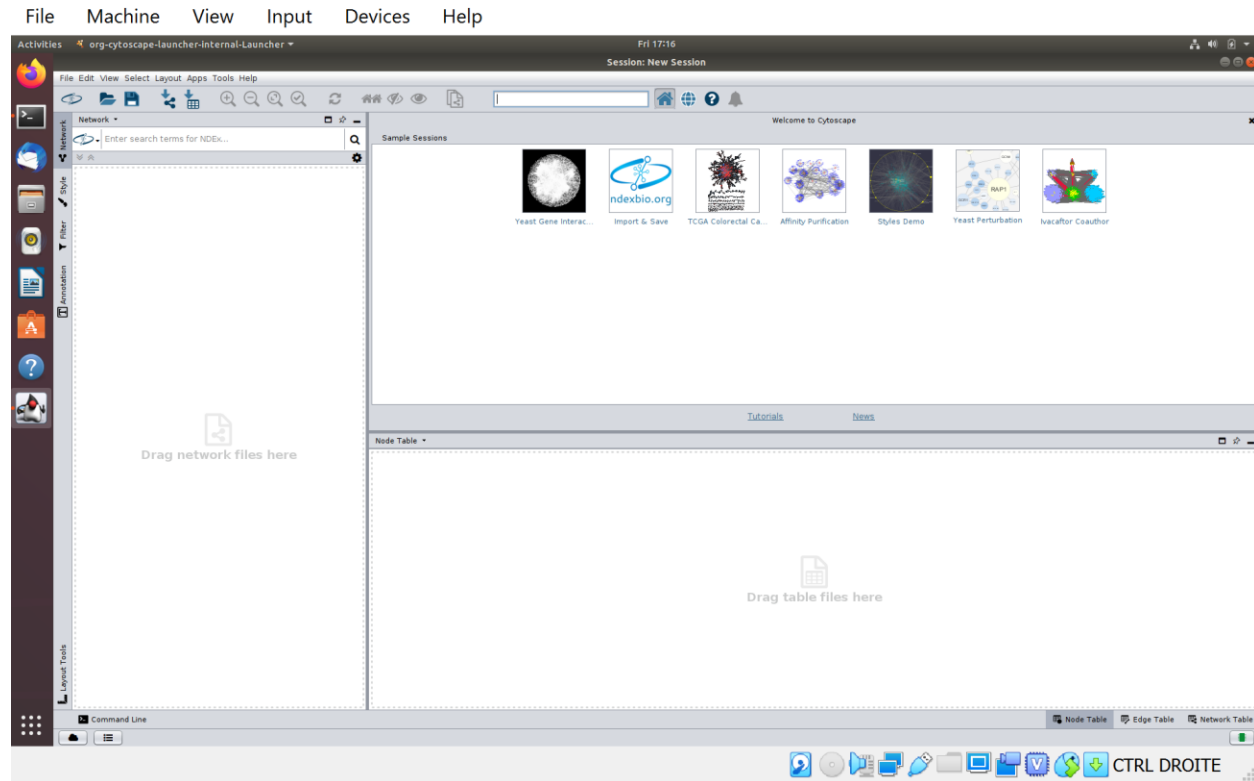
Hands-on session with Cytoscape



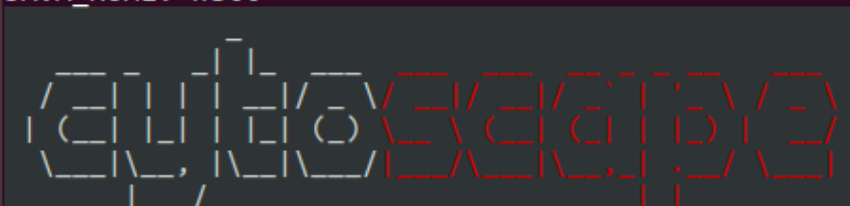
Open the terminal in your VM session, type `cytoscape.sh` and hit enter



Cytoscape will launch and you will see this message appearing on your terminal (you can always click on a shortcut, but it is useful to know how to execute simple commands on the terminal).

 CompSysBio [Running] - Oracle VM VirtualBox

```
manager@Compsysbio:~$ cytoscape.sh
karaf: JAVA_HOME not set; results may vary
karaf.base: /home/manager/Cytoscape_v3.8.2/framework
JAVA_HOME: null
```

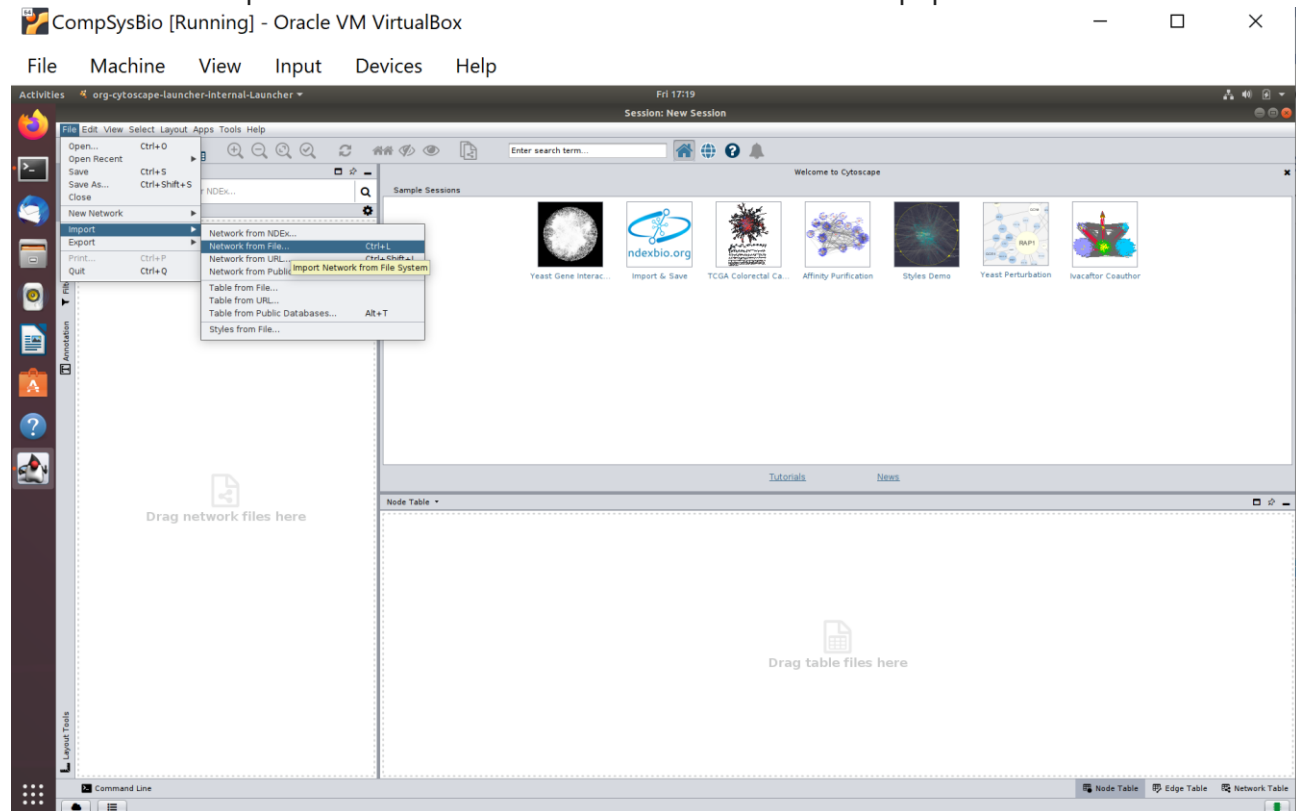


```
Cytoscape 3.8.2

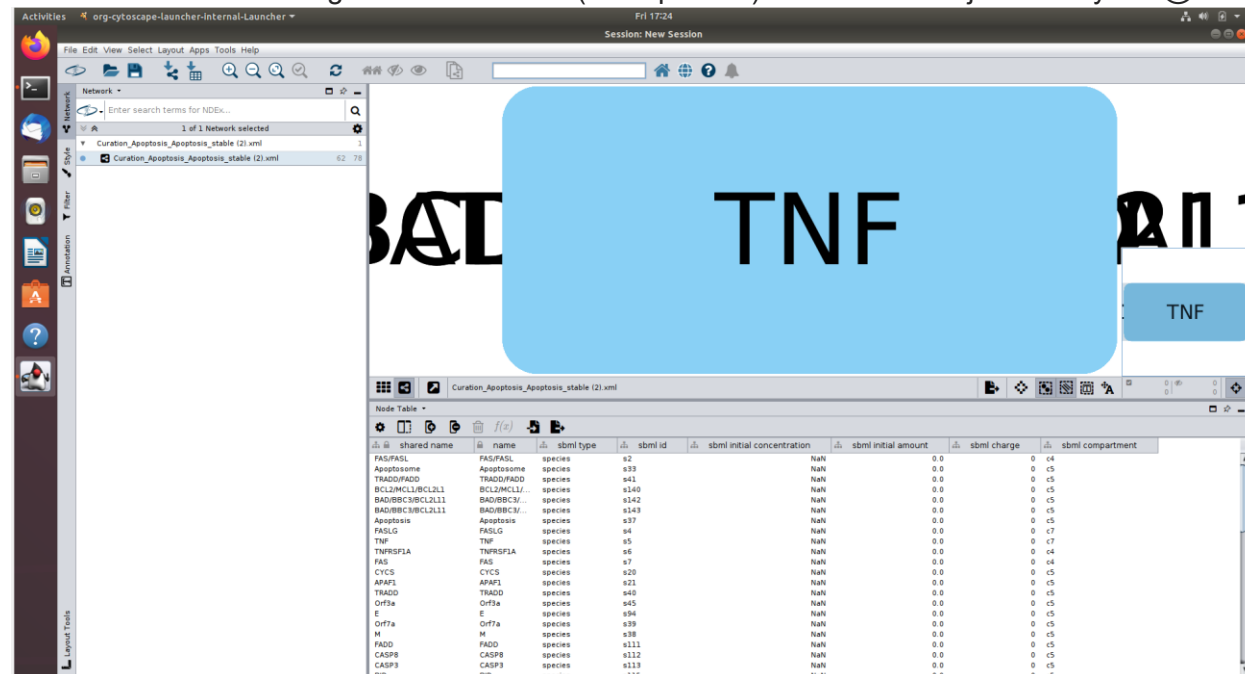
Hit '<tab>' for a list of available commands
    and '[cmd] --help' for help on a specific command.
Hit '<ctrl-d>' or 'osgi:shutdown' to shutdown Cytoscape.

karaf@Cytoscape 3.8.2(> 
```

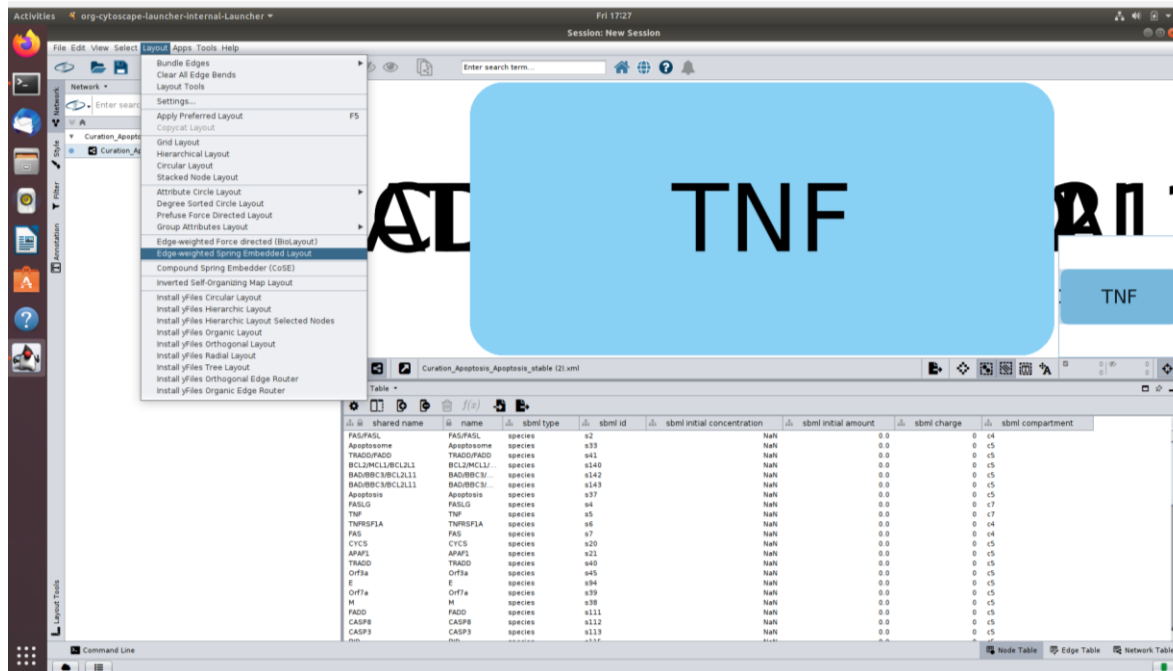
Click on File -> Import-> Network from file and select the xml file of apoptosis



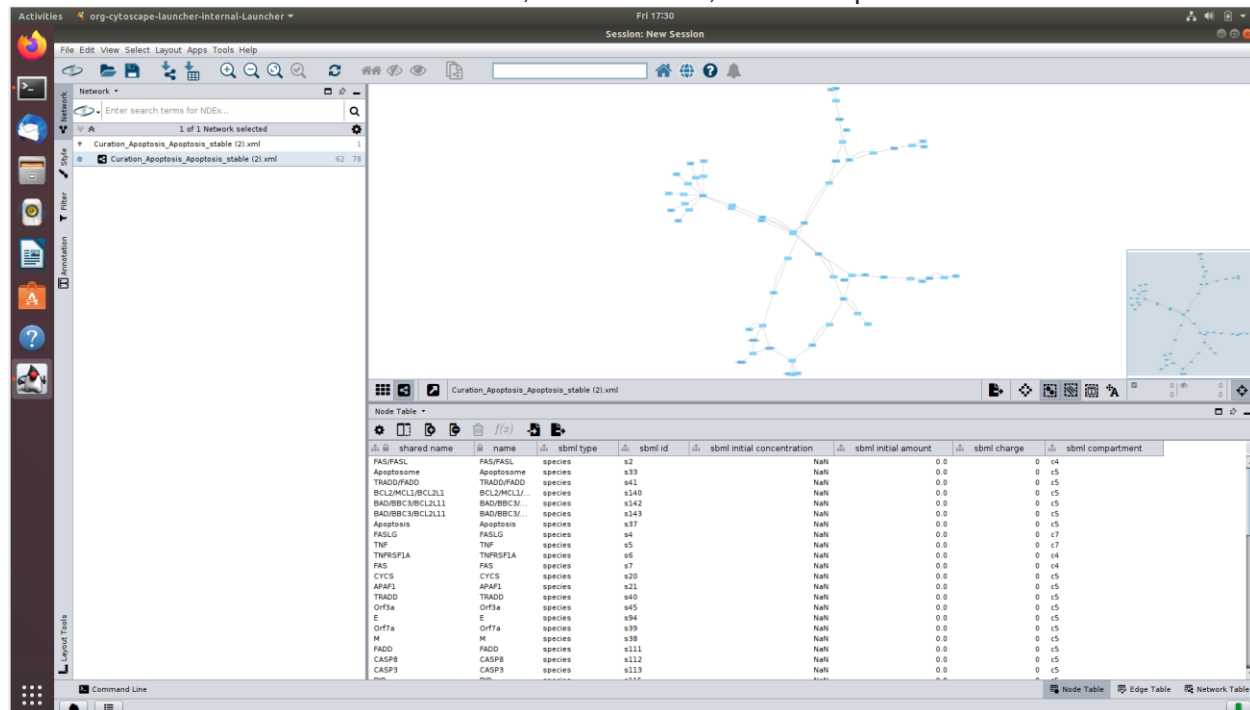
You will obtain something that look like this (don't panic!). We need to adjust the layout (☺)



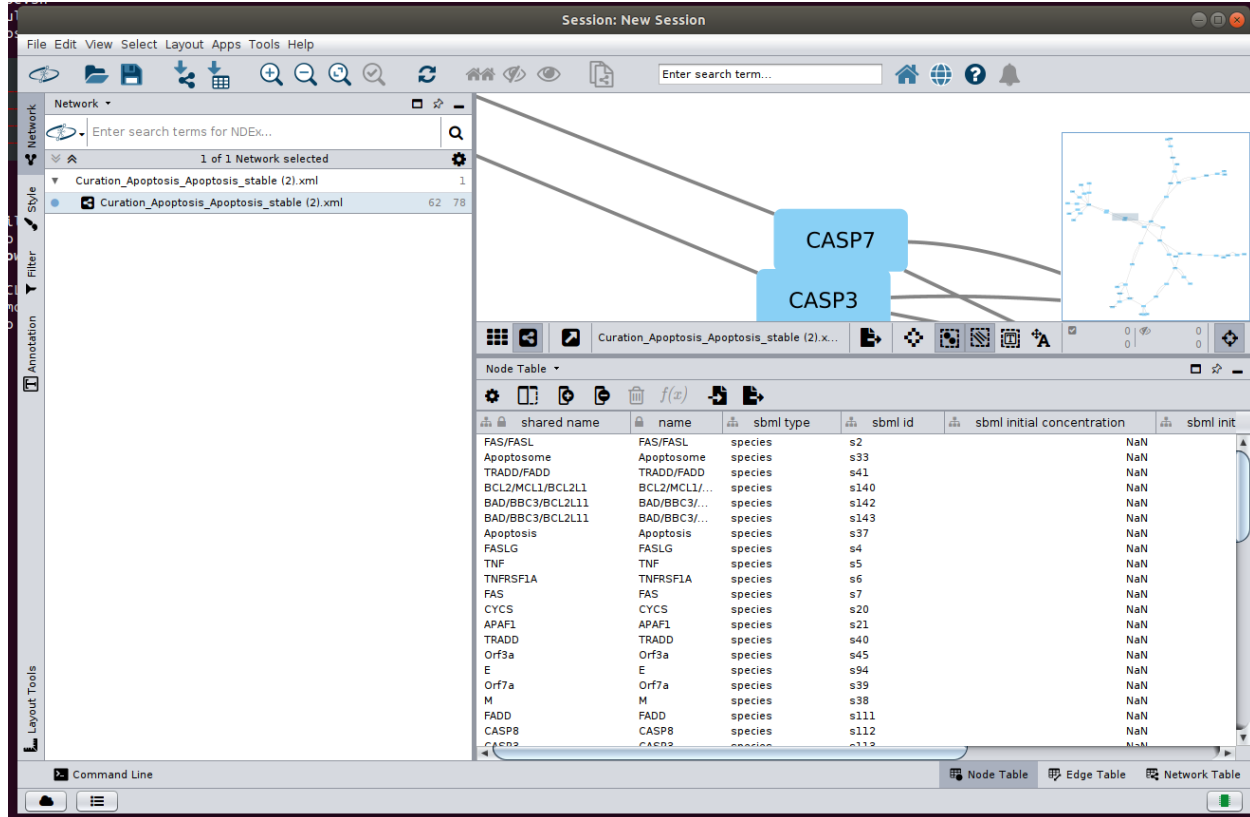
Click on Layout and Choose edge weighted spring embedded layout (you can also choose others to see what happens)



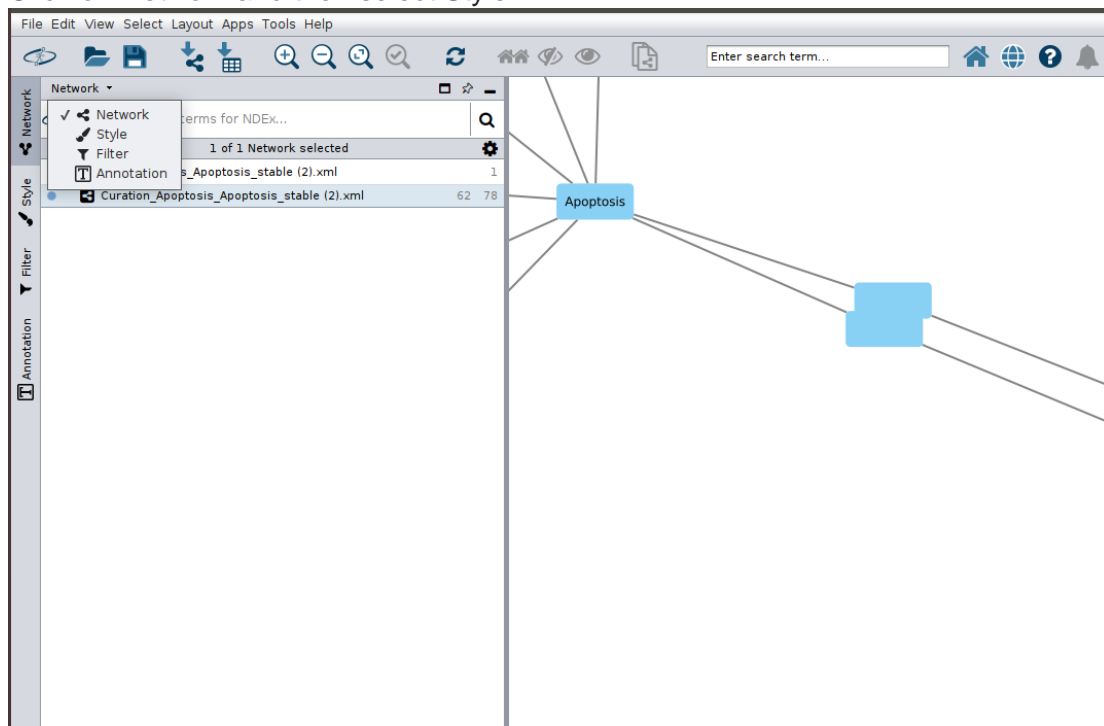
Take some time to observe the network, the attributes, the menu panel.



You can adjust the zoom with the two buttons on the top left: What do you observe regarding the nodes? Why some of them have no label?



Click on Network and then select Style



Select BioPax _SIF style for example. Take the time to try some.

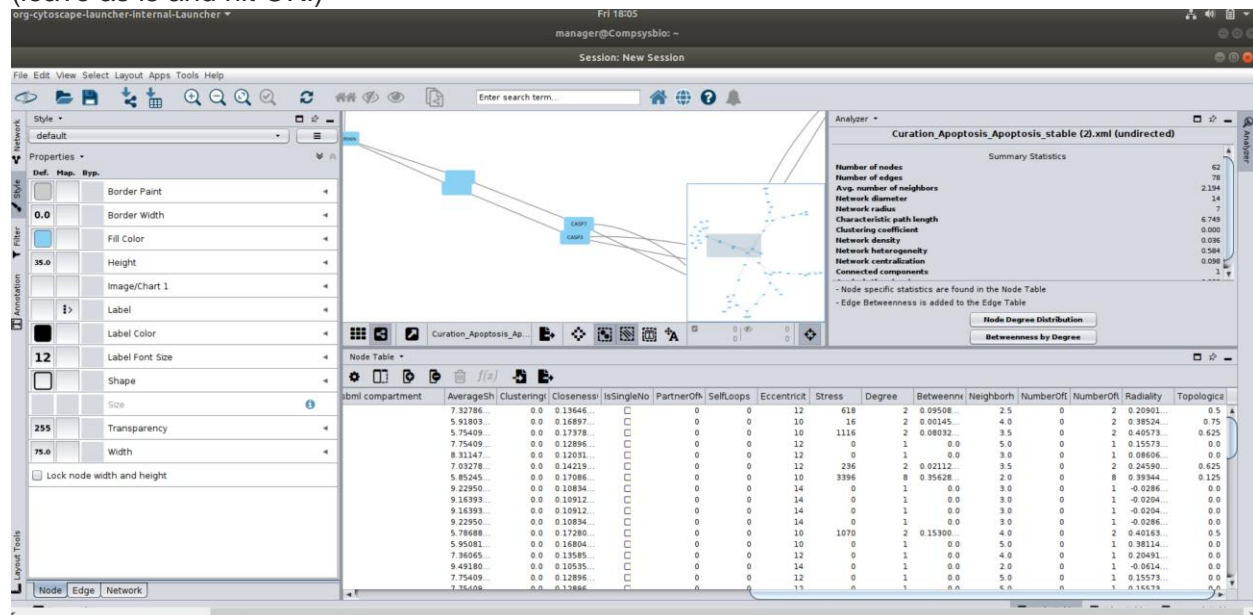
The screenshot shows the org-cytoscape-launcher-internal-launcher window. The Style menu is open, and the BioPax _SIF style is selected. The network diagram displays nodes CASP7, CASP3, and CASP8 with edges. A Node Table is visible at the bottom.

shared name	name	sbml type	sbml id	sbml initial concentration	sbml initial amount	sbml charge	sbml compartment
FAS/FASL	FAS/FASL	species	s2	NaN	0.0	0	c4
Apoptosome	Apoptosome	species	s33	NaN	0.0	0	c5
TRADD/FADD	TRADD/FADD	species	s41	NaN	0.0	0	c5
BCL2/MCL1/BCL2L1	BCL2/MCL1/BCL2L1	species	s140	NaN	0.0	0	c5
BAD/BBC3/BCL2L1	BAD/BBC3/BCL2L1	species	s142	NaN	0.0	0	c5
BAD/BBC3/BCL2L1	BAD/BBC3/BCL2L1	species	s143	NaN	0.0	0	c5
Apoptosis	Apoptosis	species	s37	NaN	0.0	0	c5
FASLG	FASLG	species	s4	NaN	0.0	0	c7
TNF	TNF	species	s5	NaN	0.0	0	c7
TNFRSF1A	TNFRSF1A	species	s6	NaN	0.0	0	c4

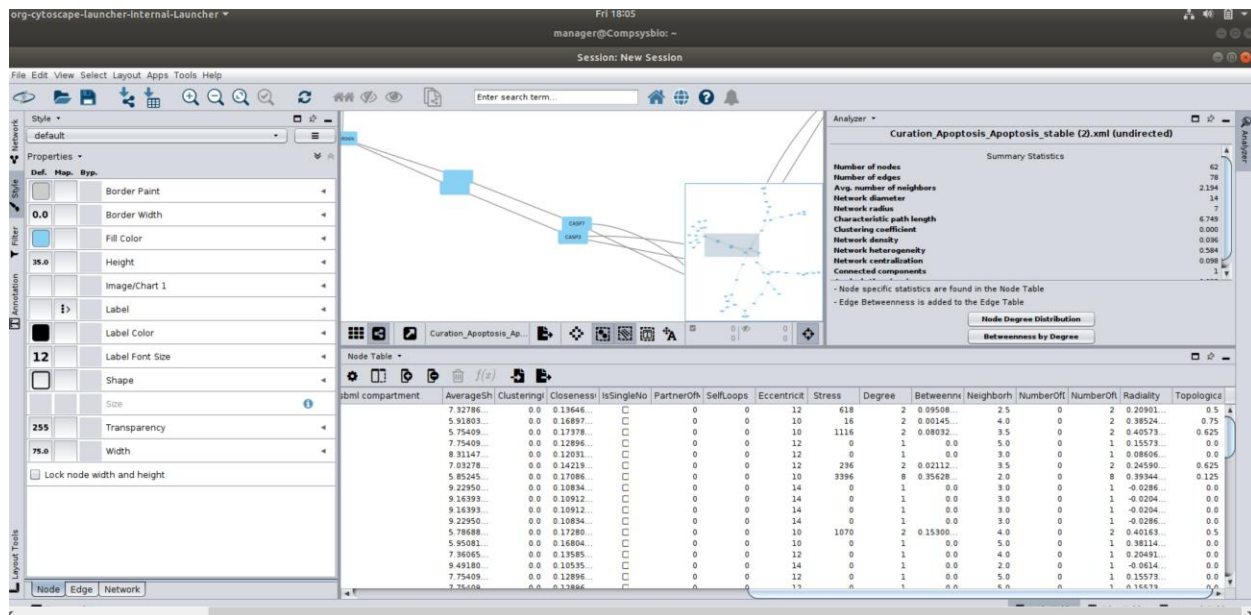
Next, we will be creating our own style using statistics from the attribute table. Let's generate some statistics! Click on Tools and then Analyze Network.

The screenshot shows the org-cytoscape-launcher-internal-launcher window. The Tools menu is open, and the Analyze Network option is selected. The network diagram displays nodes CASP7, CASP3, and CASP8 with edges.

Then you have the option to analyze your network as directed or undirected. Choose undirected (leave as is and hit OK!)



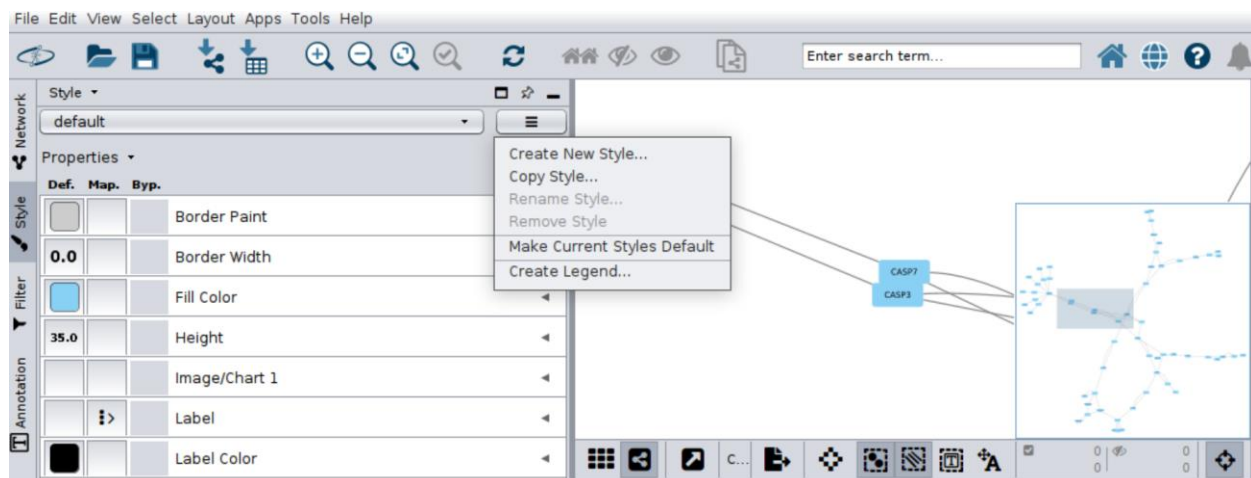
A new panel will open and on the same time in the table with attributes new columns will be added. Move your cursor to examine the columns and also click on the elements of the window with the metrics to observe what they look like.



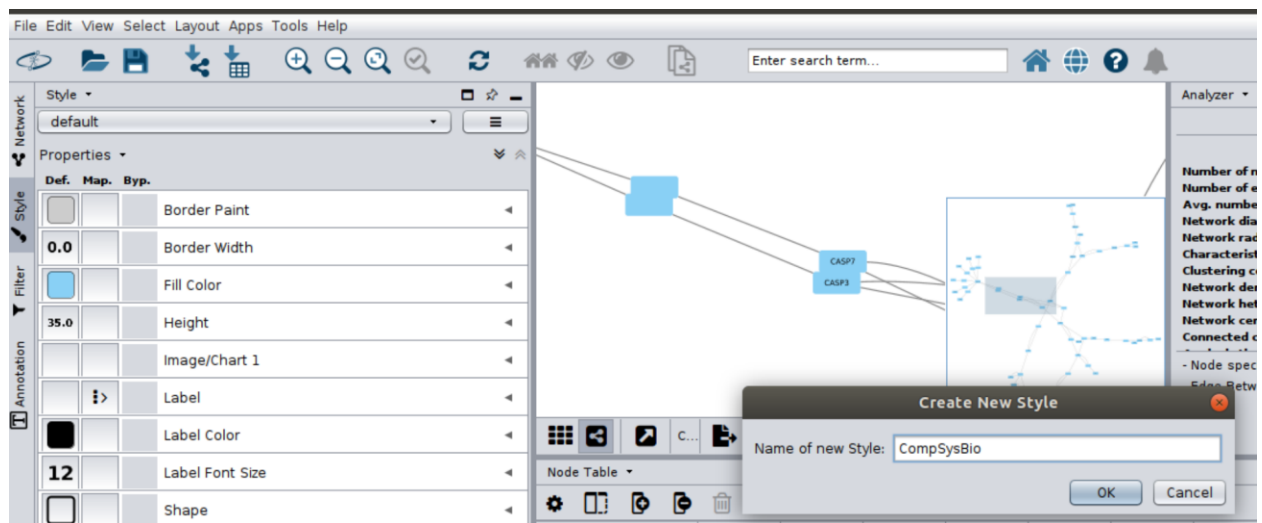
Click on the Degree tab twice to get nodes rearranged from the highest to the lowest degree of connectivity.



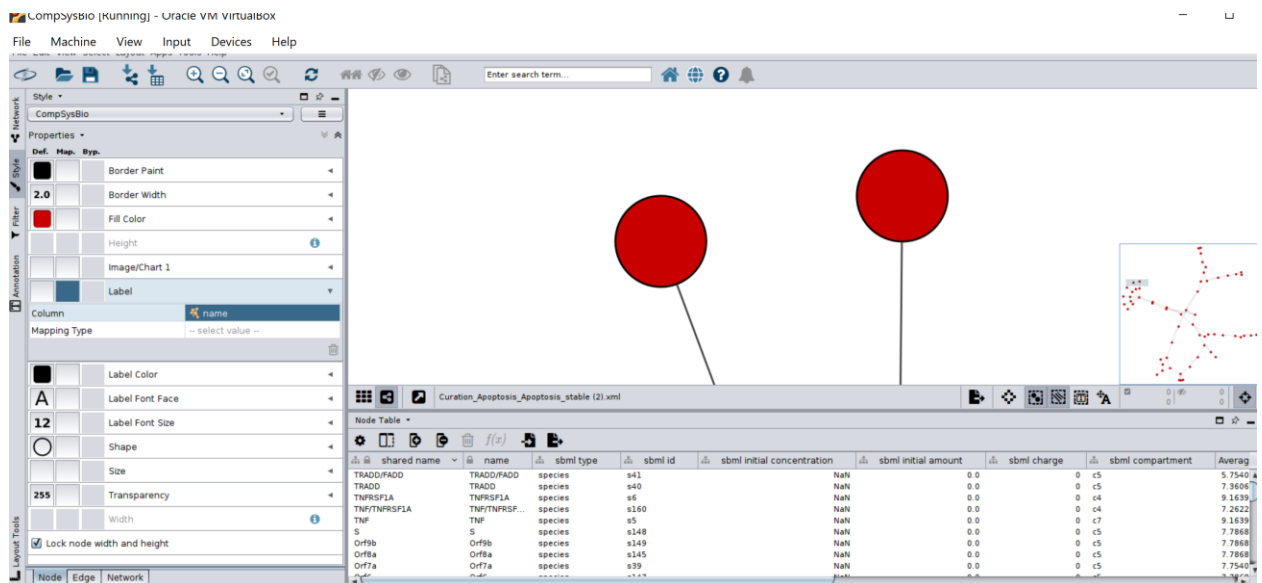
Now we are ready to create our own style! Click on the square box with the three dashes and select from the menu the Create New Style option:



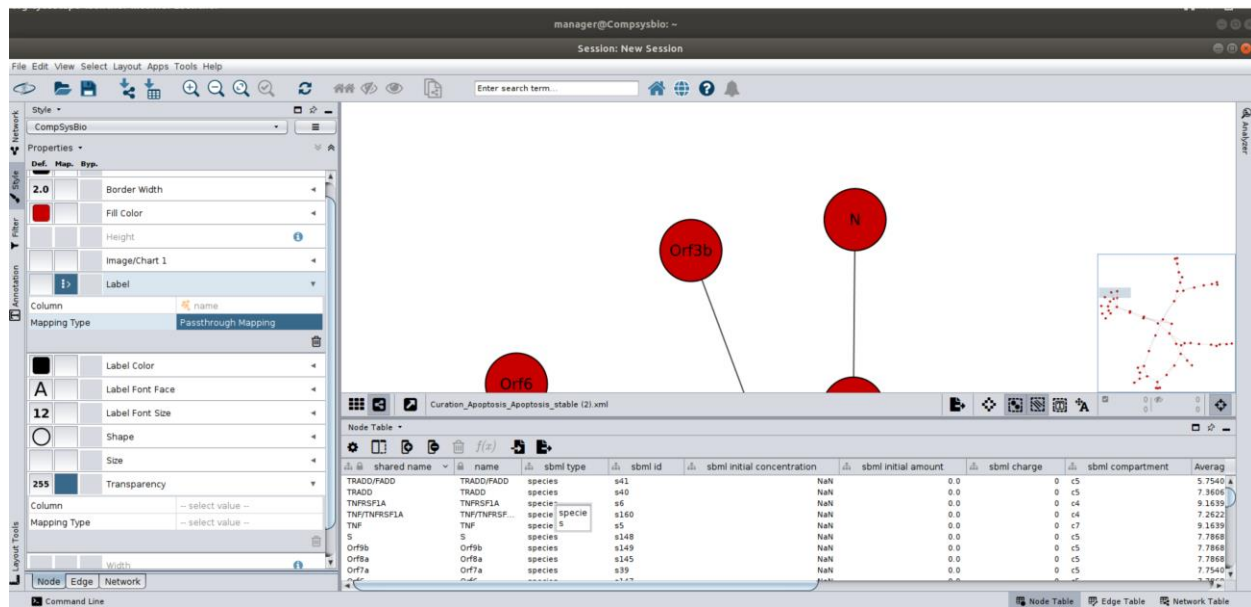
A box will appear demanding you to name your new style. Name it CompSysBio (or whatever you would like) and hit OK.



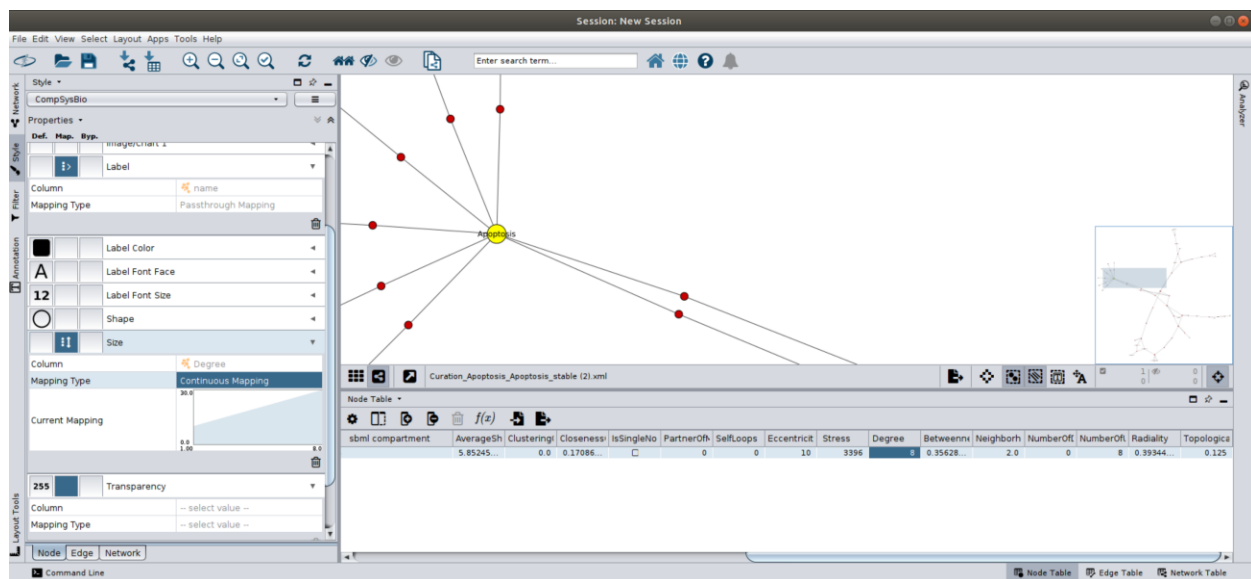
The new style will appear but as you see it has very basic elements. For example, labels are missing! If you click on a node this information still exists in the attribute table, still it is not visible on the network. Go to the properties panel, find the Label tab and click on the middle square. As a column you will select name from the drop-down menu:



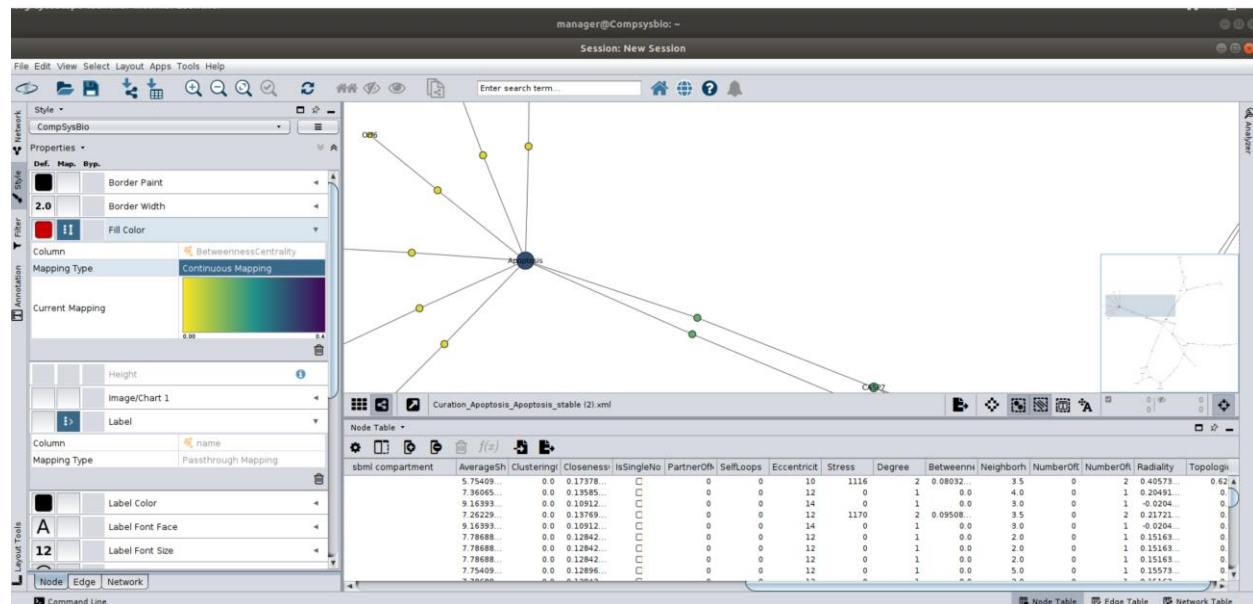
and for the Mapping type: Passthrough Mapping. Your labels now should appear now 😊



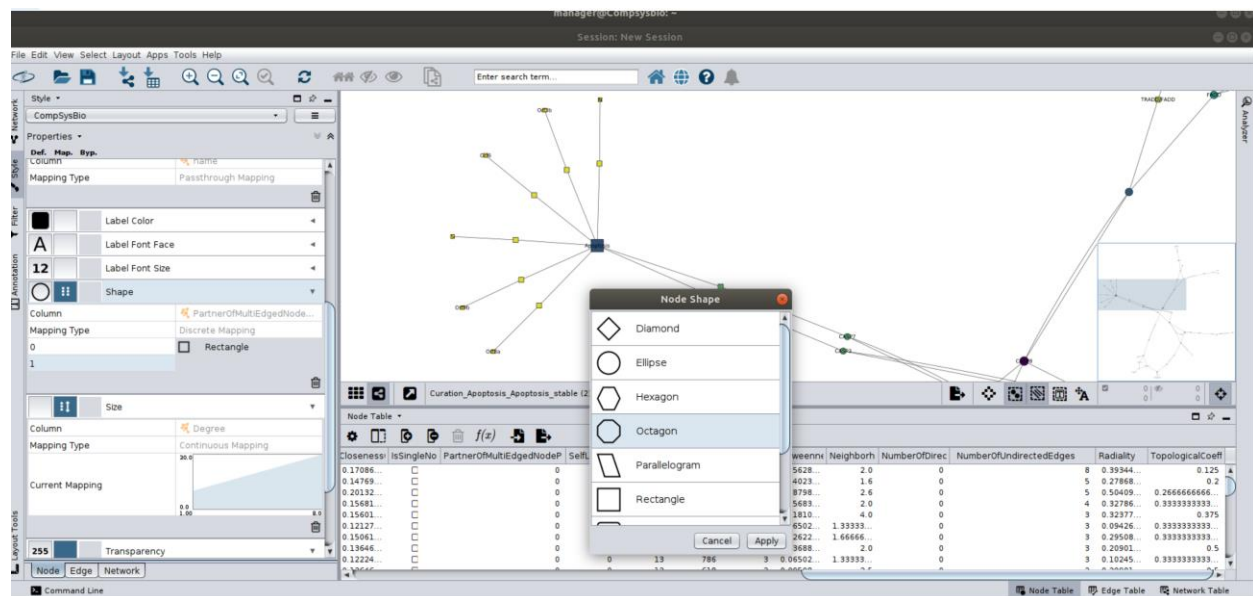
Good job! Let's change now the size – we will change the node size to make it proportional to the degree of connectivity. Like that we could highlight some hubs (if there are any). You will select Size in the left panel, then for column we will chose Degree and Continuous Mapping for the Mapping type. You should see now changes in the nodes size. In the example below we have clicked on Apoptosis which has the highest degree in the network and is therefore the biggest node.



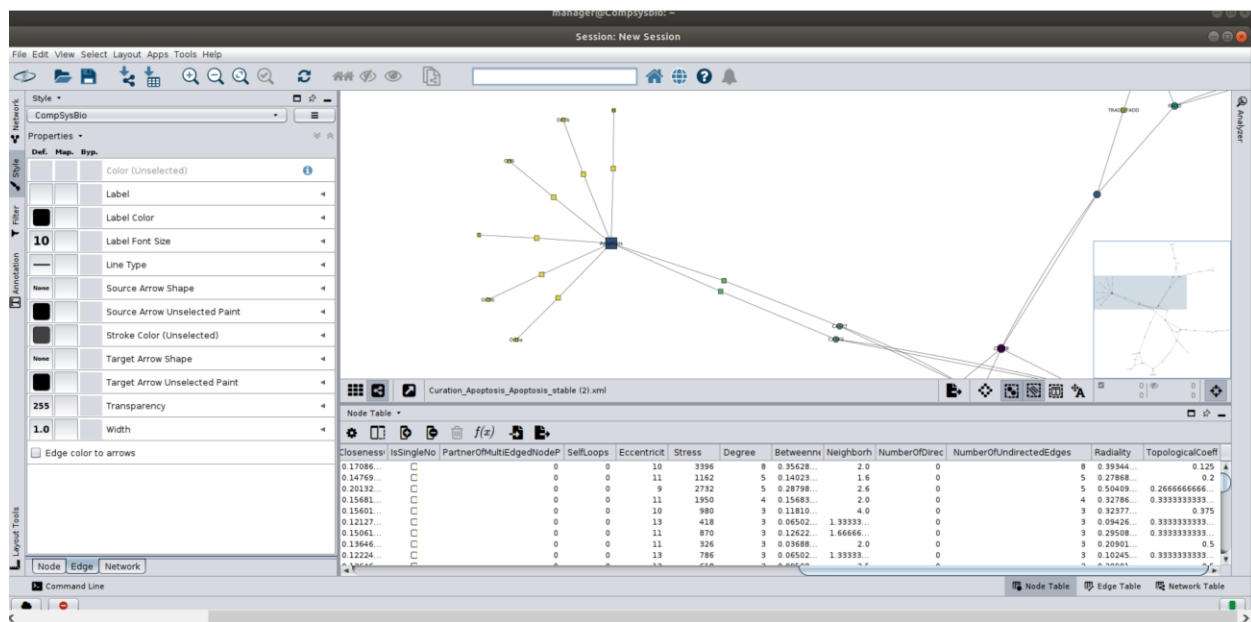
Now we will change the color of the nodes. We will select Fill Color, as column we will select another metric from the attribute table (here we use Betweenness Centrality) and Continuous Mapping.

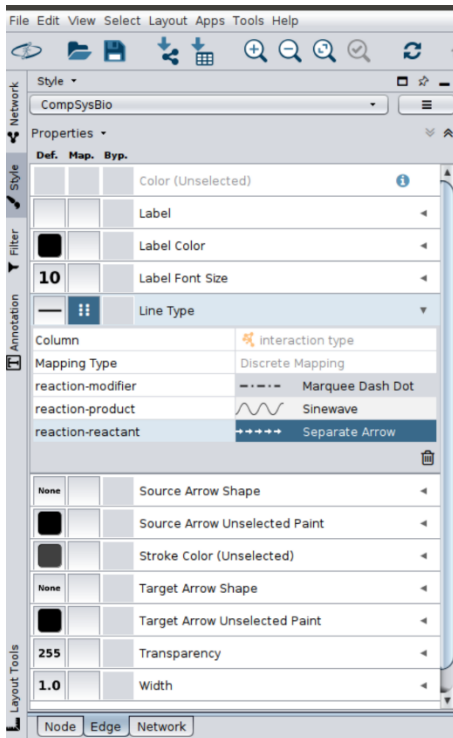


We can also change the Shape of the nodes! Here we select As Column the Partner of MultiEdgeNode and this time we select the Discrete Mapping. In Discrete Mapping we need to set an attribute to every discrete value. For zero we use the Rectangle, while for 1 we use the Octagon.

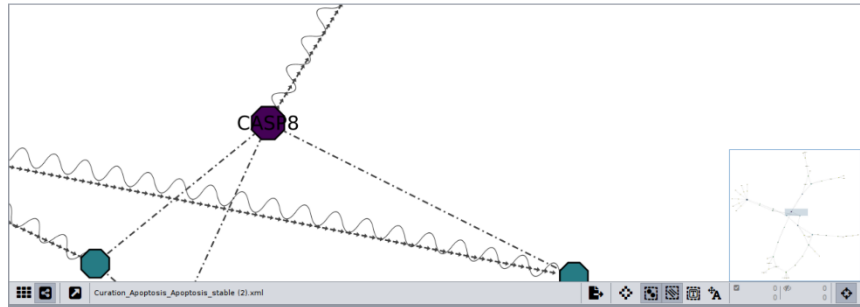


You can also click on the bottom panel on Edges to change the visual style of edges.





Here we have selected to change the line type according to the interaction type (column value). We selected Discrete Mapping and chose different line types for the three different reaction categories.



You can also modify the width and the color! Try it on your own!

Lastly, you can click on the Network at the bottom of the panel and play with the background paint etc! Here is an (ugly) example!

